What is claimed is:

1. A method of structure-based identification of compounds which potentially bind to complement receptor type 2 (CR2) proteins or to a complex of CR2 and its ligand, comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only); and,

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å; and,

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a).

2. The method of Claim 1, wherein said step of identifying comprises selecting candidate compounds that potentially bind to and activate CR2.

3. The method of Claim 1, wherein said method further comprises:

c. selecting candidate compounds of (b) that inhibit the binding of CR2 to its ligand.

4. The method of Claim 3, wherein said step (c) of selecting comprises:

i. contacting said candidate compound identified in step (b) with CR2 or a fragment thereof and a CR2 ligand or a fragment thereof under conditions in which a CR2-CR2 ligand complex can form in the absence of said candidate compound; and

ii. measuring the binding affinity of said CR2 or fragment thereof to said CR2 ligand or fragment thereof; wherein a candidate inhibitor compound is selected as a compound that inhibits the binding of CR2 to its ligand when there is a decrease in the binding affinity of said CR2 or fragment thereof for said CR2 ligand or fragment thereof, as compared to in the absence of said candidate inhibitor compound.

5. The method of Claim 3, wherein said ligand is selected from the group consisting of C3d, CD23, and Epstein Barr Virus (EBV) gp350/220, or CR2-binding fragments thereof.

6. The method of Claim 3, wherein said ligand is a gp350/220 viral membrane protein from EBV or a CR2-binding fragment thereof.

7. The method of Claim 3, wherein said CR2 protein or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:6.

8. The method of Claim 1, wherein said method further comprises:

c. selecting candidate compounds that stabilizes a complex of CR2 with its ligand.

9. The method of Claim 8, wherein step (c) of selecting comprises:

i. contacting said candidate compound identified in step (b) with a CR2-CR2 ligand complex, wherein said CR2-CR2 ligand complex comprises CR2 or a fragment thereof and a CR2 ligand, or a fragment thereof;

ii. measuring the stability of said CR2-CR2 ligand complex of (i), wherein a candidate stabilizer compound is selected as a compound that stabilizes the CR2-CR2 ligand complex when there is an increase in the stability of the said complex as compared to in the absence of said candidate stabilizer compound.

10. The method of Claim 8, wherein said ligand is selected from the group consisting of C3d and CD23.

11. The method of Claim 8, wherein said CR2 protein or fragment thereof comprises an amino acid sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:6.

12. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the SCR2 domain of said CR2.

13. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the interface between the SCR1 and SCR2 domains of CR2.

14. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the dimer interface between two CR2 proteins.

15. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the interface between CR2 and C3d, C3, a CR2-binding fragment of C3 containing C3d, or a fragment thereof.

16. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the B strand and the B-C loop of CR2 SCR2 comprising the segment: G79-G80-Y81-K82-I83-R84-G85-S86-T87-P88-Y89.

17. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to a site on the B strand of CR2 SCR2 comprising position K100.

18. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to a segment of CR2 SCR2 comprising V130-F131-P132-L133.

19. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to a segment of CR2 SCR2 comprising the fragment T101-N102-F103.

20. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to the loop between helix 2-3 of C3d comprising the segment Q68-P69-S70-S71.

21. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to Helix 5 of C3d comprising the segment S104-Q105-V106-L107-C108-G109-A110-V111-K112-W113-L114-I115-L116-E117-K118-Q119-K120-P121-D122.

22. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to Helix 7of C3d comprising the segment N170-S171-L172-P173-G174-S175-I176-T177-K178-A179-G180-D181-F182-L183-E184-A185.

23. The method of Claim 1, wherein said step of identifying comprises identifying candidate compounds for binding to amino acid residues at positions 84 and 86 of an amino acid sequence selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:6.

24. The method of Claim 1, wherein said step of identifying comprises directed drug design.

25. The method of Claim 1, wherein said step of identifying comprises random drug design.

26. The method of Claim 1, wherein said step of identifying comprises grid-based drug design.

27. The method of Claim 1, wherein said step of identifying comprises computational screening of one or more databases of chemical compounds.

28. A method to identify a compound that inhibits the complement receptor type 2 (CR2)-dependent infection of a host cell by Epstein Barr Virus (EBV), comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. contacting said candidate compound identified in step (b) with a cell that expresses CR2 or a ligand binding fragment thereof and an Epstein Barr Virus

(EBV) particle under conditions in which said EBV particle can bind to CR2 and infect said cell in the absence of said candidate compound; and

d. measuring the intracellular EBV titer of said cell; wherein a candidate inhibitor compound is selected as a compound that inhibits the EBV titer in said cell, as compared to in the absence of said candidate inhibitor compound.

29. A method to identify a compound that inhibits the binding of CD23 to complement receptor type 2 (CR2), comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c contacting said candidate compound identified in step (b) with a first cell expressing CR2 or a ligand binding fragment thereof and a second cell expressing a CD23 protein or fragment thereof under conditions in which said CD23

protein or fragment thereof and said CR2 or said ligand binding fragment thereof can bind in the absence of said candidate compound: and

d. measuring a biological activity induced by the interaction of CD23 and CR2 in said first or second cell; wherein a candidate inhibitor compound is selected as a compound that inhibits said biological activity as compared to in the absence of said candidate inhibitor compound.

30. The method of Claim 29, wherein said biological activity is IgE isotype switching in said first cell.

31. A method to identify a compound that inhibits the binding of C3d, C3 or another CR2-binding fragment of C3 containing C3d or a portion thereof, to complement receptor type 2 (CR2), comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. contacting said candidate compound identified in step (b) with a cell expressing CR2 or a fragment thereof and C3d, C3, a CR2-binding fragment of C3

containing C3d, or a fragment thereof, under conditions in which said C3d, said C3, said CR2-binding fragment of C3 containing C3d, or a fragment thereof, can bind to CR2 or the fragment thereof and enhance cell activation in the absence of said candidate compound; and

d. measuring the activation of said cell; wherein a candidate inhibitor compound is selected as a compound that inhibits cell activation, as compared to in the absence of said candidate inhibitor compound.

32. The method of Claim 31, wherein said cell is selected from the group consisting of a B cell, a T cell, a thymocyte, an epithelial cell, and a mast cell.

33. The method of Claim 31, wherein cell activation is measured by a method selected from the group consisting of: measurement of cytokine production by the cell, measurement of calcium mobilization in the cell, measurement of lyn tyrosine kinase activity in the cell, measurement of phosphatidylinositol 3' kinase activity in the cell, measurement of activation of NF-κB, measurement of activation of MAP kinases, measurement of phosphorylation of CD19 in the cell, and measurement of activation of protein kinase C (PKC) in the cell.

34. A method to inhibit complement receptor type 2 (CR2)-dependent human immunodeficiency virus-1 (HIV-1) infection of cells in a patient, comprising administering to a patient infected with HIV-1 an inhibitor compound that inhibits the binding of C3d, C3 or another CR2-binding fragment of C3 containing C3d or a portion thereof, -opsonized HIV-1 to B cells, follicular dendritic cells, T cells or macrophages in said patient, said inhibitor compound being selected by the steps of:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify

a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. contacting said candidate compound identified in step (b) with a B cell or follicular dendritic cell expressing CR2 or a fragment thereof and C3d, C3, a CR2-binding fragment of C3 containing C3d, or a fragment thereof, under conditions in which said C3d, said C3, said CR2-binding fragment of C3 containing C3d, or said fragment thereof, can bind to CR2 and enhance B cell activation or follicular dendritic cell activation in the absence of said candidate compound;

d. measuring the activation of said B cell or said follicular dendritic cell, wherein a candidate inhibitor compound is selected as a compound that inhibits B cell activation or follicular dendritic cell activation, as compared to in the absence of said candidate inhibitor compound.

35. A method of preparing a vaccine, comprising linking a compound that increases B cell activation to an antigen to form said vaccine, wherein said compound is selected by the steps of:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å; and,

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. contacting said candidate compound identified in step (b) with a B cell expressing CR2 or a fragment thereof and with C3d, C3, a CR2-binding fragment of

C3 containing C3d, or a fragment thereof, under conditions in which said C3d, said C3, said CR2-binding fragment of C3 containing C3d, or said fragment thereof, can bind to and activate CR2 in the absence of said candidate compound;

d. measuring the activation of said B cell; wherein a candidate compound for use in a vaccine is selected as a compound that increases B cell activation, as compared to in the absence of said candidate compound.

36. A drug delivery system, comprising:

a. a drug; and,

b. a portion of a CR2 protein selected from the group consisting of:

i. a portion comprising positions on strand B and the B-C loop of SCR2 including: G79-G80-Y81-K82-I83-R84-G85-S86-T87-P88-Y89;

ii. a portion comprising position K100 on the B strand of CR2;

iii. a portion comprising positions: V130-F131-P132-L133; and,

iv. a portion comprising any combination of portions (i)-(iii);

wherein said drug is linked to said portion of CR2.

37. An antibody that selectively binds to CR2, wherein said antibody binds to a portion of CR2 selected from the group consisting of:

a. the interface between the SCR1 and SCR2 domains of CR2;

b. the dimer interface between two CR2 proteins; and,

c. the interface between CR2 and C3d.

38. The antibody of Claim 37, wherein said antibody binds to an interface between CR2 and C3d at a site selected from the group consisting of:

a. the B strand and the B-C loop of CR2 SCR2 comprising the segment: G79-G80-Y81-K82-I83-R84-G85-S86-T87-P88-Y89;

b. the B strand of CR2 SCR2 comprising position K100;

c. a segment of CR2 SCR2 comprising V130-F131-P132-L133; and,

d. a segment of CR2 SCR2 comprising T101-N102-F103.

39. A crystal comprising complement receptor type 2 (CR2) in complex with C3d, wherein the CR2 consists of SEQ ID NO:4, and wherein the C3d consists of SEQ ID NO:7, wherein the crystal effectively diffracts X-rays for the determination of the atomic coordinates of the CR2 in complex with C3d to a resolution of greater than 2.0 Å, and wherein said crystal has a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 A.

40. A therapeutic composition that, when administered to an animal, enhances B cell responses in said animal, said therapeutic composition comprising a compound that stimulates the activity of a complement receptor type 2 (CR2), said compound being identified by the method comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. synthesizing said candidate compound; and

d. selecting candidate compounds that bind to and activate CR2.

41. A therapeutic composition that, when administered to an animal, inhibits the biological activity of complement receptor type 2 (CR2) in said animal, said therapeutic composition comprising a compound that inhibits the activity of a complement receptor type 2 (CR2), said compound being identified by the method comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. identifying a candidate compound for binding to said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify a compound structure that binds to said three dimensional structure of said CR2 SCR 1-2 region;

c. synthesizing said candidate compound; and

d. selecting candidate compounds that inhibit the biological activity of CR2.

42. The therapeutic composition of Claim 41, wherein said compounds inhibit the formation of a complex between CR2 and a CR2 ligand.

43. The therapeutic composition of Claim 42, wherein said ligand is selected from the group consisting of C3d, C3, CR2-binding fragments of C3 containing C3d, CD23 and Epstein Barr Virus (EBV), and CR2-binding fragments thereof.

44. The therapeutic composition of Claim 41, wherein said compound inhibits the activation of CR2.

45. A method of preparing complement receptor type 2 (CR2) proteins having modified biological activity, comprising:

a. providing a three dimensional structure of a CR2 short consensus repeat (SCR) 1-2 region selected from the group consisting of:

i. a structure defined by atomic coordinates of a three dimensional structure of a crystalline CR2 SCR1-2 region in complex with C3d;

ii. a structure defined by atomic coordinates selected from the group consisting of:

(1) atomic coordinates represented in a table selected from the group consisting of Table 2 (CR2-C3d) and Table 3 (CR2 only);

(2) atomic coordinates that define a three dimensional structure, wherein at least 50% of said structure has an average root-mean-square deviation (RMSD) from backbone atoms in secondary structure elements in at least one domain of a three dimensional structure represented by said atomic coordinates of (1) of equal to or less than about 1.0Å; and

iii. a structure defined by atomic coordinates derived from CR2 protein molecules arranged in a crystalline manner in a space group R32 so as to form a unit cell of dimensions a=b=170.5Å, c=173.8 Å;

b. analyzing said three dimensional structure to the three-dimensional structure of said CR2 SCR 1-2 region by performing structure based drug design with said structure of (a) to identify at least one site in said structure contributing to the biological activity of CR2; and

c. modifying said at least one site in a CR2 protein to alter the biological activity of said CR2 protein.

46. An isolated protein comprising a mutant C3d, wherein said protein comprises an amino acid sequence that differs from SEQ ID NO:7 by an amino acid substitution selected from the group consisting of: a non-asparagine amino acid residue at position 115, and a non-leucine amino acid residue at position 116; wherein said C3d mutant protein has reduced binding to complement receptor type 2 (CR2), as compared to a wild-type C3d protein.

47. The isolated C3d mutant protein of Claim 46, wherein said mutant protein comprises an amino acid sequence selected from the group consisting of SEQ ID NO:8 and SEQ ID NO:9.